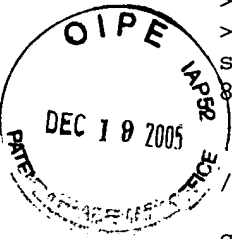# APPENDIX A

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
>US20040081980 SEQ ID NO:10                  642 aa vs.
>US 10/674,636 SEQ ID NO:2                   581 aa
scoring matrix: BLOSUM50, gap penalties: -12/-2
86.9% identity;        Global alignment score: 3612


               10        20        30        40        50        60
/tmp/s MVVVPFTIPFDSSVWLLQKLNSPWRMTVDYHTLNQAVTLIIAAVLGVASLLEQGFSRAIW
         :    :   .  ..: : .                 ::.   .::        . :
SEQ    M---PQGLTSSASQWCF-------------------FLILQPLLG----------HRQW
            10                              20


               70        80        90        100       110       120
/tmp/s ENRESLSKVCVSQGPSRPLACATNGDIKVQGGPSAEGPQRNTRLGWIQGKQVTVLGSPVP
                   :  .                 :::::::::::::::::::::::::::
SEQ    -------------GKT---------------GPSAEGPQRNTRLGWIQGKQVTVLGSPVP
                    30                              40        50


               130       140       150       160       170       180
/tmp/s VNVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYP
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    VNVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYP
          60        70        80        90        100       110


               190       200       210       220       230       240
/tmp/s KFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVV
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    KFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVV
          120       130       140       150       160       170


               250       260       270       280       290       300
/tmp/s QYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVS
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    QYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVS
          180       190       200       210       220       230


               310       320       330       340       350       360
/tmp/s SLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLR
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    SLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLR
          240       250       260       270       280       290


               370       380       390       400       410       420
/tmp/s TKPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMK
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    TKPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMK
          300       310       320       330       340       350


               430       440       450       460       470       480
/tmp/s EAPEVLSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFV
         ::::.::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ    EAPEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFV
          360       370       380       390       400       410
```

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```
            490       500       510       520       530       540
/tmp/s  VPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVM
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ     VPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVM
        420       430       440       450       460       470


            550       560       570       580       590       600
/tmp/s  FEGATEEEKLLSRKMMKYWATFARTGNPNGNDLFLWPAYNLTEQYLQLDLNMSLGQRLKE
        ::::::::::::::::::::::::::::::::::: ::::::::::::::::::::::::::
SEQ     FEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKE
        480       490       500       510       520       530


            610       620       630       640
/tmp/s  PRVEFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP
        :::.::::::::::::::::::::::::::::::::::::::::
SEQ     PRVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP
        540       550       560       570       580
```

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